

Patent Application US 07/599,543A

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Opperman, Hermann
Ozkaynak, Engin
Rueger, David C.
Kuberasampath, Thangavel
- (ii) TITLE OF INVENTION: Osteogenic Protein
- (iii) NUMBER OF SEQUENCES: 11
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Lahive & Cockfield
(B) STREET: 60 State Street
(C) CITY: Boston
(D) STATE: Massachusetts
(E) COUNTRY: U.S.A.
(F) ZIP: 02109
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette, 3.5 inch,
720kb storage
- (B) COMPUTER: IBM XT
- (C) OPERATING SYSTEM: DOS 3.30
- (D) SOFTWARE: Word Perfect 5.0
- (vi) CURRENT APPLICATION DATA:
(B) FILING DATE: 18-Oct-90
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 569,920
(B) FILING DATE: 20-Aug-90
(C) APPLICATION NUMBER: US 315,342
(D) FILING DATE: 23-Feb-89
(E) APPLICATION NUMBER: US 422,699
(F) FILING DATE: 17-Oct-89

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remarks, please
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308-4224
-meredith

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lines. Abbreviate, & place on
one line.

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

81	Ala	Ala	Arg	Pro	Leu	Lys	Arg	Arg	Gln
82	1				5				
83	Pro	Lys	Lys	Thr	Asn	Glu	Leu	Pro	His
84	10					15			
85	Pro	Asn	Lys	Leu	Pro	Gly	Ile	Phe	Asp
86	20						25		
87	Asp	Gly	His	Gly	Ser	Arg	Gly	Arg	Glu
88			30					35	
89	Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val
90				40					45
91	Arg	Phe	Arg	Asp	Leu	Gly	Trp	Leu	Asp
92					50				
93	Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser
94	55					60			
95	Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ala
96		65					70		
97	Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala
98			75					80	
99	Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu
100				85					90
101	Val	His	Leu	Met	Lys	Pro	Asp	Val	Val
102					95				
103	Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys
104	100					105			
105	Leu	Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr
106		110					115		

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139 Asp Ser Ser Asn Asn Val Ile Leu Arg
140 120 125
141 Lys His Arg Asn Met Val Val Lys Ala
142 130 135
143 Cys Gly Cys His

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146 (2) INFORMATION FOR SEQ ID NO:2:
147 (i) SEQUENCE CHARACTERISTICS:
148 (A) LENGTH: 1930 base pairs
149 (B) TYPE: nucleic acid
150 (C) STRANDEDNESS: single
151 (D) TOPOLOGY: linear
152 (ii) MOLECULE TYPE: cDNA
153 (iii) HYPOTHETICAL: no
154 (iv) ANTI-SENSE: no
155 (vi) ORIGINAL SOURCE:
156 (A) ORGANISM: Bovinae
157 (F) TISSUE TYPE: bone
158 (vii) IMMEDIATE SOURCE:
159 (A) LIBRARY: mouse embryo

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160 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
161
162 GGAATTCGCG TGCCAGGCAC AGGTGCGCCG TCTGGTCCTC 40
163 CCCGTCTGGC GTCAGCCGAG CCCGACCAGC TACCAGTGGG 80
164 TGC GCGCCCG CTGAAAGTCC GAG ATG GCT ATG CGT 115
165 Met Ala Met Arg
166 1
167 CCC GGG CCA CTC TGG CTA TTG GGC CTT GCT CTG 148
168 Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu
169 5 10 15
170 TGC GCG CTG GGA GGC GGC CAC GGT CCC GGT CCC 181
171 Cys Ala Leu Gly Gly Gly His Gly Pro Gly Pro
172 20 25
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205 CCG CAC ACC TGT CCC CAG CGT CGC CTG GGA GCG 214
206 Pro His Thr Cys Pro Gln Arg Arg Leu Gly Ala
207 30 35
208 CGC GAC CGG GAC ATG CAG CGT GAA ATC CTG CCG 247
209 Arg Asp Arg Asp Met Gln Arg Glu Ile Leu Pro
210 40 45
211 GTG CTC GGG CTA CCG GGA CGC CCC GAC CCC GTG 280
212 Val Leu Gly Leu Pro Gly Arg Pro Asp Pro Val

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213	50	55	
214	CAC AAC CCG CCG CTG CCC GGC ACG CAG CGT GCG	313	
215	His Asn Pro Pro Leu Pro Gly Thr Gln Arg Ala		
216	60	65	70
217	CCC CTC TTC ATG TTG GAC CTA TAC CAC GCC ATG	346	
218	Pro Leu Phe Met Leu Asp Leu Tyr His Ala Met		
219	75	80	
220	ACC GAT GAC GAC GAC GGC GGG CCA CCA CAG GCT	379	
221	Thr Asp Asp Asp Asp Gly Gly Pro Pro Gln Ala		
222	85	90	
223	CAC TTA GGC CGT GCC GAC CTG GTC ATG AGC TTC	412	
224	His Leu Gly Arg Ala Asp Leu Val Met Ser Phe		
225	95	100	
226	GTC AAC ATG GTG GAA CGC GAC CGT ACC CTG GGC	445	
227	Val Asn Met Val Glu Arg Asp Arg Thr Leu Gly		
228	105	110	
229	TAC CAG GAG CCA CAC TGG AAG GAA TTC CAC TTT	478	
230	Tyr Gln Glu Pro His Trp Lys Glu Phe His Phe		
231	115	120	125
232	GAC CTA ACC CAG ATC CCT GCT GGG GAG GCT GTC	511	
233	Asp Leu Thr Gln Ile Pro Ala Gly Glu Ala Val		
234	130	135	
235	ACA GCT GCT GAG TTC CGG ATC TAC AAA GAA CCC	544	
236	Thr Ala Ala Glu Phe Arg Ile Tyr Lys Glu Pro		
237	140	145	
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271 AGC ACC CAC CCG CTC AAC ACA ACC CTC CAC ATC 577

272 Ser Thr His Pro Leu Asn Thr Thr Leu His Ile

273 150 155

274 AGC ATG TTC GAA GTG GTC CAA GAG CAC TCC AAC 610

275 Ser Met Phe Glu Val Val Gln Glu His Ser Asn

276 160 165

277 AGG GAG TCT GAC TTG TTC TTT TTG GAT CTT CAG 643

278 Arg Glu Ser Asp Leu Phe Phe Leu Asp Leu Gln

279 170 175 180

280 ACG CTC CGA TCT GGG GAC GAG GGC TGG CTG GTG 676

281 Thr Leu Arg Ser Gly Asp Glu Gly Trp Leu Val

282 185 190

283 CTG GAC ATC ACA GCA GCC AGT GAC CGA TGG CTG 709

284 Leu Asp Ile Thr Ala Ala Ser Asp Arg Trp Leu

285 195 200

286 CTG AAC CAT CAC AAG GAC CTG GGA CTC CGC CTC 742

287 Leu Asn His His Lys Asp Leu Gly Leu Arg Leu

288 205 210

289 TAT GTG GAA ACC GCG GAT GGG CAC AGC ATG GAT 775

290 Tyr Val Glu Thr Ala Asp Gly His Ser Met Asp

291 215 220

292 CCT GGC CTG GCT GGT CTG CTT GGA CGA CAA GCA 808

293 Pro Gly Leu Ala Gly Leu Leu Gly Arg Gln Ala

294 225 230 235

295 CCA CGC TCC AGA CAG CCT TTC ATG GTA ACC TTC 841

296 Pro Arg Ser Arg Gln Pro Phe Met Val Thr Phe

297 240 245

298 TTC AGG GCC AGC CAG AGT CCT GTG CGG GCC CCT 874

299 Phe Arg Ala Ser Gln Ser Pro Val Arg Ala Pro

300 250 255

301 CGG GCA GCG AGA CCA CTG AAG AGG AGG CAG CCA 907

302 Arg Ala Ala Arg Pro Leu Lys Arg Arg Gln Pro

303 260 265

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AAG	AAA	ACG	AAC	GAG	CTT	CCG	CAC	CCC	AAC	AAA	940
Lys	Lys	Thr	Asn	Glu	Leu	Pro	His	Pro	Asn	Lys	
	270					275					
CTC	CCA	GGG	ATC	TTT	GAT	GAT	GGC	CAC	GGT	TCC	973
Leu	Pro	Gly	Ile	Phe	Asp	Asp	Gly	His	Gly	Ser	
	280				285					290	
CGC	GGC	AGA	GAG	GTT	TGC	CGC	AGG	CAT	GAG	CTC	1006
Arg	Gly	Arg	Glu	Val	Cys	Arg	Arg	His	Glu	Leu	
			295						300		
TAC	GTC	AGA	TTC	CGT	GAC	CTT	GGC	TGG	CTG	GAC	1039
Tyr	Val	Arg	Phe	Arg	Asp	Leu	Gly	Trp	Leu	Asp	
			305					310			
TGG	GTC	ATC	GCC	CCC	CAG	GGC	TAC	TCT	GCC	TAT	1072
Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser	Ala	Tyr	
		315				320					
TAC	TGT	GAG	GGG	GAG	TGT	GCT	TTC	CCA	CTG	GAC	1105
Tyr	Cys	Glu	Gly	Glu	Cys	Ala	Phe	Pro	Leu	Asp	
		325				330					
TCC	TGT	ATG	AAC	GCC	ACC	AAC	CAT	GCC	ATC	TTG	1138
Ser	Cys	Met	Asn	Ala	Thr	Asn	His	Ala	Ile	Leu	
	335				340					345	
CAG	TCT	CTG	GTG	CAC	CTG	ATG	AAG	CCA	GAT	GTT	1171
Gln	Ser	Leu	Val	His	Leu	Met	Lys	Pro	Asp	Val	
			350						355		
GTC	CCC	AAG	GCA	TGC	TGT	GCA	CCC	ACC	AAA	CTG	1204
Val	Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys	Leu	
			360					365			
AGT	GCC	ACC	TCT	GTG	CTG	TAC	TAT	GAC	AGC	AGC	1237
Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr	Asp	Ser	Ser	
		370				375					
AAC	AAT	GTC	ATC	CTG	CGT	AAA	CAC	CGT	AAC	ATG	1270
Asn	Asn	Val	Ile	Leu	Arg	Lys	His	Arg	Asn	Met	
		380				385					

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GTG GTC AAG GCC TGT GGC TGC CAC 1294
Val Val Lys Ala Cys Gly Cys His
390 400
TGAGGCCCGG CCCAGCATCC TGCTTCTACT ACCTTACCAT 1334
CTGGCCGGGC CCCTCTCCAG AGGCAGAAAC CCTTCTATGT 1374
TATCATAGCT CAGACAGGGG CAATGGGAGG CCCTTCACTT 1414
CCCCTGGCCA CTCCTGCTA AAATTCTGGT CTTTCCCAGT 1454
TCCTCTGTCC TTCATGGGGT TTCGGGGCTA TCACCCCGCC 1494
CTCTCCATCC TCCTACCCCA AGCATAGACT GAATGCACAC 1534
AGCATCCCAG AGCTATGCTA ACTGAGAGGT CTGGGGTCAG 1574
CACTGAAGGC CCACATGAGG AAGACTGATC CTTGGCCATC 1614
CTCAGCCCAC AATGGCAAAT TCTGGATGGT CTAAGAAGCC 1654
CTGGAATTCT AAACATAGATG ATCTGGGCTC TCTGCACCAT 1694
TCATTGTGGC AGTTGGGACA TTTTATAGGTA TAACAGACAC 1734
ATACACTTAG ATCAATGCAT CGCTGTACTC CTTGAAATCA 1774
GAGCTAGCTT GTTAGAAAAA GAATCAGAGC CAGGTATAGC 1814
GGTGCATGTC ATTAATCCCA GCGCTAAAGA GACAGAGACA 1854
GGAGAATCTC TGTGAGTTCA AGGCCACATA GAAAGAGCCT 1894
GTCTCGGGAG CAGGAAAAAA AAAAAAACG GAATTC 1930

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(2) INFORMATION FOR SEQ ID NO:3:

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425 (i) SEQUENCE CHARACTERISTICS:
426 (A) LENGTH: 139 amino acids
427 (B) TYPE: amino acid
428 (D) TOPOLOGY: linear
429 (ii) MOLECULE TYPE: protein
430 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
431

432	Ala	Val	Arg	Pro	Leu	Arg	Arg	Arg	Gln
433	1				5				
434	Pro	Lys	Lys	Ser	Asn	Glu	Leu	Pro	Gln
435	10					15			

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469	Ala	Asn	Arg	Leu	Pro	Gly	Ile	Phe	Asp
470		20					25		
471	Asp	Val	His	Gly	Ser	His	Gly	Arg	Gln
472			30					35	
473	Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val
474				40					45
475	Ser	Phe	Gln	Asp	Leu	Gly	Trp	Leu	Asp
476					50				
477	Trp	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser

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478	55					60			
479	Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ser
480		65					70		
481	Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala
482			75					80	
483	Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu
484				85					90
485	Val	His	Leu	Met	Lys	Pro	Asn	Ala	Val
486					95				
487	Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys
488	100					105			
489	Leu	Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr
490		110					115		
491	Asp	Ser	Ser	Asn	Asn	Val	Ile	Leu	Arg
492			120					125	
493	Lys	Ala	Arg	Asn	Met	Val	Val	Lys	Ala
494				130					135
495	Cys	Gly	Cys	His	Delete punctuation				
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497									

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1956 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

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535 (D) TOPOLOGY: linear
536 (ii) MOLECULE TYPE: cDNA
537 (iii) HYPOTHETICAL: no
538 (iv) ANTI-SENSE: no
539 (vi) ORIGINAL SOURCE:
540 (A) ORGANISM: Bovinae
541 (F) TISSUE TYPE: bone
542 (vii) IMMEDIATE SOURCE:
543 (A) LIBRARY: human hippocampus
544 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
545
546 GGAATTCCGG CCACAGTGGC GCCGGCAGAG CAGGAGTGGC 40
547 TGGAGGAGCT GTGGTTGGAG CAGGAGGTGG CACGGCAGGG 80
548 CTGGAGGGCT CCCTATGAGT GGCGGAGACG GCCCAGGAGG 120
549 CGCTGGAGCA ACAGCTCCCA CACCGCACCA AGCGGTGGCT 160
550 GCAGGAGCTC GCCCATCGCC CCTGCGCTGC TCGGACCGCG 200
551 GCCACAGCCG GACTGGCGGG TACGGCGGGC ACAGAGGCAT 240
552 TGGCCGAGAG TCCCAGTCCG CAGAGTAGCC CCGGCCTCGA 280
553 GGCGGTGGCG TCCCGGTCCT CTCCGTCCAG GAGCCAGGAC 320
554 AGGTGTCCCG CGGCGGGGCT CCAGGGACCG CGCCTGAGGC 360
555 CGGCTGCCCC CCCGTCCCGC CCGCCCCGCG CGCCCGCCGC 400
556 CCGCCGAGCC CAGCCTCCTT GCCGTCGGGG CGTCCCCAGG 440
557 CCCTGGGTCTG GCCGCGGAGC CGATGCGCGC CCGCTGAGCG 480
558 CCCCAGCTGA GCGCCCCCGG CCTGCC ATG ACC GCG CTC 518
559 Met Thr Ala Leu
560 1
561 CCC GGC CCG CTC TGG CTC CTG GGC CTG GCG CTA 551
562 Pro Gly Pro Leu Trp Leu Leu Gly Leu Ala Leu
563 5 10 15
564 TGC GCG CTG GGC GGG GGC GGC CCC GGC CTG CGA 584
565 Cys Ala Leu Gly Gly Gly Gly Pro Gly Leu Arg
566 20 25
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601 CCC CCG CCC GGC TGT CCC CAG CGA CGT CTG GGC 617
602 Pro Pro Pro Gly Cys Pro Gly arg Arg Leu Gly
603 30 35
604 GCG CGC GAC CGG GAC GTG CAG CGC GAG ATC CTG 650
605 Ala Arg Asp Arg Asp Val Gln Arg Glu Ile Leu
606 40 45
607 GCG GTG CTC GGG CTG CCT GGG CGG CCC CGG CCC 683
608 Ala Val Leu Gly Leu Pro Gly Arg Pro Arg Pro
609 50 55
610 CGC GCG CCA CCC GCC GCC TCC CGG CTG CCC GCG 716
611 Arg Ala Pro Pro Ala Ala Ser Arg Leu Pro Ala
612 60 65 70
613 TCC GCG CCG CTC TTC ATG CTG GAC CTG TAC CAC 749
614 Ser Ala Pro Leu Phe Met Leu Asp Leu Tyr His
615 75 80
616 CGC ATG GCC GGC GAC GAC GAC GAG GAC GGC GCC 782
617 Arg Met Ala Gly Asp Asp Asp Glu Asp Gly Ala
618 85 90
619 GCG GAG GCC CTG GGC CGC GCC GAC CTG GTC ATG 815
620 Ala Glu Ala Leu Gly Arg Ala Asp Leu Val Met
621 95 100
622 AGC TTC GTT AAC ATG GTG GAG CGA GAC CGT GCC 848
623 Ser Phe Val Asn Met Val Glu Arg Asp Arg Ala
624 105 110
625 CTG GGC CAC CAG GAG CCC CAT TGG AAG GAG TTC 881
626 Leu Gly His Gln Glu Pro His Trp Lys Glu Phe
627 115 120 125
628 CGC TTT GAC CTG ACC CAG ATC CCG GCT GGG GAG 914
629 Arg Phe Asp Leu Thr Gln Ile Pro Ala Gly Glu
630 130 135
631 GCG GTC ACA GCT GCG GAG TTC CGG ATT TAC AAG 947
632 Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys
633 140 145
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667 GTG CCC AGC ATC CAC CTG CTC AAC AGG ACC CTC 980
668 Val Pro Ser Ile His Leu Leu Asn Arg Thr Leu
669 150 155
670 CAC GTC AGC ATG TTC CAG GTG GTC CAG GAG CAG 1013
671 His Val Ser Met Phe Gln Val Val Gln Glu Gln
672 160 165
673 TCC AAC AGG GAG TCT GAC TTG TTC TTT TTG GAT 1046
674 Ser Asn Arg Glu Ser Asp Leu Phe Phe Leu Asp
675 170 175 180
676 CTT CAG ACG CTC CGA GCT GGA GAC GAG GGC TGG 1079
677 Leu Gln Thr Leu Arg Ala Gly Asp Glu Gly Trp
678 185 190
679 CTG GTG CTG GAT GTC ACA GCA GCC AGT GAC TGC 1112
680 Leu Val Leu Asp Val Thr Ala Ala Ser Asp Cys
681 195 200
682 TGG TTG CTG AAG CGT CAC AAG GAC CTG GGA CTC 1145
683 Trp Leu Leu Lys Arg His Lys Asp Leu Gly Leu
684 205 210
685 CGC CTC TAT GTG GAG ACT GAG GAC GGG CAC AGC 1178
686 Arg Leu Tyr Val Glu Thr Glu Asp Gly His Ser
687 215 220
688 GTG GAT CCT GGC CTG GCC GGC CTG CTG GGT CAA 1211
689 Val Asp Pro Gly Leu Ala Gly Leu Leu Gly Gln

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690 225                230                235
691 CGG GCC CCA CGC TCC CAA CAG CCT TTC GTG GTC 1244
692 Arg Ala Pro Arg Ser Gln Gln Pro Phe Val Val
693                240                245
694 ACT TTC TTC AGG GCC AGT CCG AGT CCC ATC CGC 1277
695 Thr Phe Phe Arg Ala Ser Pro Ser Pro Ile Arg
696                250                255
697 ACC CCT CGG GCA GTG AGG CCA CTG AGG AGG AGG 1310
698 Thr Pro Arg Ala Val Arg Pro Leu Arg Arg Arg
699                260                265
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733 CAG CCG AAG AAA AGC AAC GAG CTG CCG CAG GCC 1343
734 Gln Pro Lys Lys Ser Asn Glu Leu Pro Gln Ala
735                270                275
736 AAC CGA CTC CCA GGG ATC TTT GAT GAC GTC CAC 1376
737 Asn Arg Leu Pro Gly Ile Phe Asp Asp Val His
738 280                285                290
739 GGC TCC CAC GGC CGG CAG GTC TGC CGT CGG CAC 1409
740 Gly Ser His Gly Arg Gln Val Cys Arg Arg His
741                295                300
742 GAG CTC TAC GTC AGC TTC CAG GAC CTC GGC TGG 1442

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743 Glu Leu Tyr Val Ser Phe Gln Asp Leu Gly Trp
744 305 310
745 CTG GAC TGG GTC ATC GCT CCC CAA GGC TAC TCG 1475
746 Leu Asp Trp Val Ile Ala Pro Gln Gly Tyr Ser
747 315 320
748 GCC TAT TAC TGT GAG GGG GAG TGC TCC TTC CCA 1508
749 Ala Tyr Tyr Cys Glu Gly Glu Cys Ser Phe Pro
750 325 330
751 CTG GAC TCC TGC ATG AAT GCC ACC AAC CAC GCC 1541
752 Leu Asp Ser Cys Met Asn Ala Thr Asn His Ala
753 335 340 345
754 ATC CTG CAG TCC CTG GTG CAC CTG ATG AAG CCA 1574
755 Ile Leu Gln Ser Leu Val His Leu Met Lys Pro
756 350 355
757 AAC GCA GTC CCC AAG GCG TGC TGT GCA CCC ACC 1607
758 Asn Ala Val Pro Lys Ala Cys Cys Ala Pro Thr
759 360 365
760 AAG CTG AGC GCC ACC TCT GTG CTC TAC TAT GAC 1640
761 Lys Leu Ser Ala Thr Ser Val Leu Tyr Tyr Asp
762 370 375
763 AGC AGC AAC AAC GTC ATC CTG CGC AAA GCC CGC 1673
764 Ser Ser Asn Asn Val Ile Leu Arg Lys Ala Arg
765 380 385
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799 AAC ATG GTG GTC AAG GCC TGC GGC TGC CAC 1703
800 Asn Met Val Val Lys Ala Cys Gly Cys His
801 390 395
802 TGAGTCAGCC CGCCCAGCCC TACTGCAGCA ATTCAGTGGC 1743
803 CGTCGTTTTA CAACGTGTGA CTGGGAAAAC CCTGGCGTTA 1783
804 CCCAACTTAA TCGCCTTGCA GCACATCCCC CTTTCGCCAG 1823
805 CTGGCTAATA GCGAAGAGGC CCCGCACCGA TCGCCCTTCC 1863
806 CAACAGTTGC GCCCCAGTGA ATGGCGAATG GCAAATTGTA 1903
807 AGCGTTAATA TTTTGTAAA ATTGCGGTTA AATTTTTT 1941
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810 (2) INFORMATION FOR SEQ ID NO:5:

811 (i) SEQUENCE CHARACTERISTICS:

812 (A) LENGTH: 98 amino acids

813 (B) TYPE: amino acid

814 (D) TOPOLOGY: linear

815 (ii) MOLECULE TYPE: protein

816 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

817
818 Cys Xaa1 Xaa2 His Glu Leu Tyr Val Xaa3 Phe
819 1 5 10
820 Xaa4 Asp Leu Gly Trp Xaa5 Asp Trp Xaa6 Ile
821 15 20
822 Ala Pro Xaa7 Gly Tyr Xaa8 Ala Tyr Tyr Cys
823 25 30
824 Glu Gly Cys Xaa9 Phe Pro Leu Xaa10 Ser Xaa11
825 35 40
826 Met Asn Ala Thr Asn His Ala Ile Xaa12 Thr
827 45 50
828 Leu Xaa13 Xaa14 Xaa15 Xaa16 Xaa17 Xaa18 Val
829 55
830 Pro Lys Xaa19 Cys Cys Ala Pro Thr Xaa20 Leu
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Xaa21 Ala Xaa22 Ser Val Leu Tyr Xaa23 Asp
70 75
Xaa24 Ser Xaa25 Asn Val Xaa26 Leu Xaa27 Lys
80 85
Xaa28 Pro Asn Met Val Val Xaa29 Ala Cys Gly
90 95
Cys His *Grenada comma*

wherein Xaa1 = (Lys or Arg); Xaa2 = (Lys or Arg);
Xaa3 = (Ser or Arg); Xaa4 = (Arg or Gln); Xaa5 =
(Gln or Leu); Xaa6 = (Ile or Val); Xaa7 = (Glu or
Gln); Xaa8 = (Ala or Ser); Xaa9 = (Ala or Ser); Xaa10
= (Asn or Asp); Xaa11 = (Tyr or Cys); Xaa12 = (Val
or Leu); Xaa13 = (His or Asn); Xaa14 = (Phe or
Leu); Xaa15 = (Ile or Met); Xaa16 = (Asn or Lys);
Xaa17 = (Glu, Asp or Asn); Xaa18 = (Thr, Ala or
Val); Xaa19 = (Pro or Ala); Xaa20 = (Gln or Lys);
Xaa21 = (Asn or Ser); Xaa22 = (Ile or Thr); Xaa23 =
(Phe or Tyr); Xaa24 = (Asp, Glu or Ser); Xaa25 =
(Ser or Asn); Xaa26 = (Ile or Asp); Xaa27 = (Lys or
Arg); Xaa28 = (Tyr, Ala or His); and Xaa29 = (Arg
or Lys).

place this
type of information
in the application
(paper form).
According to the
Sequence Rules, this
type of information
should not be
placed in the CRF.

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 437 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: no
- (iv) ANTI-SENSE: no
- (vi) ORIGINAL SOURCE:

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(A) ORGANISM: Bovinae
(F) TISSUE TYPE: bone
(vii) IMMEDIATE SOURCE:
(A) LIBRARY: human placenta
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TCC ACG GGG 9
Ser Thr Gly
1

AGC AAA CAG CGC AGC CAG AAC CGC TCC AAG ACG 42
Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr
5 10
CCC AAG AAC CAG GAA GCC CTG CGG ATG GCC AAC 75
Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn
15 20 25
GTG GCA GAG AAC AGC AGC AGC GAC CAG AGG CAG 108
Val Ala Glu Asn Ser Ser Ser Asp Gln Arg Gln
30 35
GCC TGT AAG AAG CAC GAG CTG TAT GTC AGC TTC 141
Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe
40 45
CGA GAC CTG GGC TGG CAG GAC TGG ATC ATC GCG 174
Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala
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955 CCT GAA GGC TAC GCC GCC TAC TAC TGT GAG GGG 207
956 Pro Glu Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly
957 60 65
958 GAG TGT GCC TTC CCT CTG AAC TCC TAC ATG AAC 240
959 Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn
960 70 75 80
961 GCC ACC AAC CAC GCC ATC GTG CAG ACG CTG GTC 273
962 Ala Thr Asn His Ala Ile Val Gln Thr Leu Val
963 85 90
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997 CAC TTC ATC AAC CCG GAA ACG GTG CCC AAG CCC 306
998 His Phe Ile Asn Pro Glu Thr Val Pro Lys Pro
999 95 100
1000 TGC TGT GCG CCC ACG CAG CTC AAT GCC ATC TCC 339
1001 Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile Ser
1002 105 110
1003 GTC CTC TAC TTC GAT GAC AGC TCC AAC GTC ATC 372
1004 Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
1005 115 120
1006 CTG AAG AAA TAC AGA AAC ATG GTG GTC CGG GCC 405
1007 Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala

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1008 125 130 135
1009 TGT GGC TGC CAC TAGCTCCTCC GAGAATTCAG 437
1010 Cys Gly Cys His
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1013 (2) INFORMATION FOR SEQ ID NO:7:

1014 (i) SEQUENCE CHARACTERISTICS:

1015 (A) LENGTH: 102 amino acids

1016 (B) TYPE: amino acid

1017 (D) TOPOLOGY: linear

1018 (ii) MOLECULE TYPE: protein

1019 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

1020
1021 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1022 1 5 10
1023 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1024 15 20
1025 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa
1026 25 30
1027 Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa
1028 35 40
1029 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1030 45 50 55
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1063 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
1064 60 65
1065 Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1066 70 75
1067 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1068 80 85
1069 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys
1070 90 95
1071 Xaa Cys Xaa ~~delete punctuation~~
1072 100
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1074 wherein each Xaa independently represents one of
1075 the 20 naturally occurring L-isomer, α -amino acids. ~~delete text~~
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(2) INFORMATION FOR SEQ ID NO:8:

1079 (i) SEQUENCE CHARACTERISTICS:
1080 (A) LENGTH: 97 amino acids
1081 (B) TYPE: amino acid
1082 (D) TOPOLOGY: linear
1083 (ii) MOLECULE TYPE: protein
1084 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
1085

1086 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1087 1 5 10
1088 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1089 15 20
1090 Xaa Xaa Cys Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa
1091 25 30
1092 Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
1093 35 40
1094 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

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Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

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wherein each Xaa independently represents one of
the 20 naturally occurring L-isomer, α-amino acids.

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- (2) INFORMATION FOR SEQ ID NO:9:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 136 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Pro Leu Arg Arg Arg Gln

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Pro Lys Lys Ser Asn Glu Leu Pro Gln

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Ala Asn Arg Leu Pro Gly Ile Phe Asp

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Asp Val Asn Gly Ser His Gly Arg Gln

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Val Cys Arg Arg His Glu Leu Tyr Val

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Ser Phe Gln Asp Leu Gly Trp Leu Asp

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Tyr	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser
			55					60
Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ser
			65					
Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala
70					75			
Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu
80						85		
Val	His	Leu	Met	Lys	Pro	Asn	Ala	Val
		90					95	
Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys
			100					105
Leu	Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr
				110				
Asp	Glu	Ser	Asn	Asn	Val	Ile	Leu	Arg
115					120			
Lys	Ala	Arg	Asn	Met	Val	Val	Lys	Ala
	125						130	
Cys	Gly	Cys	His					
		135						

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INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 133 amino acids

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1220 (B) TYPE: amino acid
1221 (D) TOPOLOGY: linear
1222 (ii) MOLECULE TYPE: protein
1223 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
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1225							Arg	Arg	Gln
1226							1		
1227	Pro	Lys	Lys	Ser	Asn	Glu	Leu	Pro	Gln
1228		5					10		
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1261	Ala	Asn	Arg	Leu	Pro	Gly	Ile	Phe	Asp
1262			15					20	
1263	Asp	Val	Asn	Gly	Ser	His	Gly	Arg	Gln
1264			25						30
1265	Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val
1266				35					
1267	Ser	Phe	Gln	Asp	Leu	Gly	Trp	Leu	Asp
1268	40					45			
1269	Tyr	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser
1270		50					55		
1271	Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ser
1272			60					65	

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1273	Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala
1274				70					75
1275	Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu
1276					80				
1277	Val	His	Leu	Met	Lys	Pro	Asn	Ala	Val
1278	85					90			
1279	Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys
1280		95					100		
1281	Leu	Ser	Ala	Thr	Ser	Val	Leu	Tyr	Tyr
1282			105					110	
1283	Asp	Glu	Ser	Asn	Asn	Val	Ile	Leu	Arg
1284				115					120
1285	Lys	Ala	Arg	Asn	Met	Val	Val	Lys	Ala
1286					125				

1287 Cys Gly Cys His *delete punctuation*
1288 130
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1291 (2) INFORMATION FOR SEQ ID NO:11:
1292 (i) SEQUENCE CHARACTERISTICS:
1293 (A) LENGTH: 170 amino acids
1294 (B) TYPE: amino acid
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1327 (D) TOPOLOGY: linear
1328 (ii) MOLECULE TYPE: protein
1329 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
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1331						Ser	Gln	Gln	
1332						1			
1333	Pro	Phe	Val	Val	Thr	Phe	Phe	Arg	Ala
1334		5				10			
1335	Ser	Pro	Ser	Pro	Ile	Arg	Thr	Pro	Arg
1336			15				20		
1337	Ala	Val	Arg	Pro	Leu	Arg	Arg	Arg	Gln
1338			25						30
1339	Pro	Lys	Lys	Ser	Asn	Glu	Leu	Pro	Gln
1340				35					
1341	Ala	Asn	Arg	Leu	Pro	Gly	Ile	Phe	Asp
1342	40					45			
1343	Asp	Val	Asn	Gly	Ser	His	Gly	Arg	Gln
1344		50				55			
1345	Val	Cys	Arg	Arg	His	Glu	Leu	Tyr	Val
1346			60				65		
1347	Ser	Phe	Gln	Asp	Leu	Gly	Trp	Leu	Asp
1348			70						75
1349	Tyr	Val	Ile	Ala	Pro	Gln	Gly	Tyr	Ser
1350				80					
1351	Ala	Tyr	Tyr	Cys	Glu	Gly	Glu	Cys	Ser
1352	85					90			
1353	Phe	Pro	Leu	Asp	Ser	Cys	Met	Asn	Ala
1354		95				100			
1355	Thr	Asn	His	Ala	Ile	Leu	Gln	Ser	Leu
1356			105					110	
1357	Val	His	Leu	Met	Lys	Pro	Asn	Ala	Val
1358			115						120
1359	Pro	Lys	Ala	Cys	Cys	Ala	Pro	Thr	Lys
1360				125					

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Leu Ser Ala Thr Ser Val Leu Tyr Tyr

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Asp Glu Ser Asn Asn Val Ile Leu Arg

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Lys Ala Arg Asn Met Val Val Lys Ala

150 165

Cys Gly Cys His ~~delete~~ punctuation
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Raw Sequence Listing

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Patent Application US 07/599,543A

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07/599,543A

The "5" + "9" errors made the

"Entered + Calc. Seq."

Line	Erro	Original text
✓23	Extr	720kb storage
✓70	Extr	- 2-
✓136	Wron	- 3-
✓143	Wron	Cys Gly Cys His.
✓79	Ente	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
✓466	Wron	- 8-
✓495	Wron	Cys Gly Cys His.
✓430	Ente	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
✓532	Extr	- 9-
544	Entered and Calc. Seq. Length differ	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
818	Wrong Amino Acid Designator	Cys Xaa1 Xaa2 His Glu Leu Tyr Val Xaa3 Phe
818	Wrong Amino Acid Designator	Cys Xaa1 Xaa2 His Glu Leu Tyr Val Xaa3 Phe
818		Cys Xaa1 Xaa2 His Glu Leu Tyr Val Xaa3 Phe
820		Xaa4 Asp Leu Gly Trp Xaa5 Asp Trp Xaa6 Ile
820		Xaa4 Asp Leu Gly Trp Xaa5 Asp Trp Xaa6 Ile
820		Xaa4 Asp Leu Gly Trp Xaa5 Asp Trp Xaa6 Ile
822		Ala Pro Xaa7 Gly Tyr Xaa8 Ala Tyr Tyr Cys
822		Ala Pro Xaa7 Gly Tyr Xaa8 Ala Tyr Tyr Cys
824		Glu Gly Cys Xaa9 Phe Pro Leu Xaa10 Ser Xaa11
824		Glu Gly Cys Xaa9 Phe Pro Leu Xaa10 Ser Xaa11
824		Glu Gly Cys Xaa9 Phe Pro Leu Xaa10 Ser Xaa11
826		Met Asn Ala Thr Asn His Ala Ile Xaa12 Thr
828		Leu Xaa13 Xaa14 Xaa15 Xaa16 Xaa17 Xaa18 Val
828		Leu Xaa13 Xaa14 Xaa15 Xaa16 Xaa17 Xaa18 Val
828		Leu Xaa13 Xaa14 Xaa15 Xaa16 Xaa17 Xaa18 Val
828		Leu Xaa13 Xaa14 Xaa15 Xaa16 Xaa17 Xaa18 Val
828		Leu Xaa13 Xaa14 Xaa15 Xaa16 Xaa17 Xaa18 Val
828		Leu Xaa13 Xaa14 Xaa15 Xaa16 Xaa17 Xaa18 Val
830		Pro Lys Xaa19 Cys Cys Ala Pro Thr Xaa20 Leu
830		Pro Lys Xaa19 Cys Cys Ala Pro Thr Xaa20 Leu
862		- 14-
865	Wrong Amino Acid Designator	Xaa21 Ala Xaa22 Ser Val Leu Tyr Xaa23 Asp
865	Wrong Amino Acid Designator	Xaa21 Ala Xaa22 Ser Val Leu Tyr Xaa23 Asp
865	Wrong Amino Acid Designator	Xaa21 Ala Xaa22 Ser Val Leu Tyr Xaa23 Asp
867	Wrong Amino Acid Designator	Xaa24 Ser Xaa25 Asn Val Xaa26 Leu Xaa27 Lys
867	Wrong Amino Acid Designator	Xaa24 Ser Xaa25 Asn Val Xaa26 Leu Xaa27 Lys
867	Wrong Amino Acid Designator	Xaa24 Ser Xaa25 Asn Val Xaa26 Leu Xaa27 Lys
867	Wrong Amino Acid Designator	Xaa24 Ser Xaa25 Asn Val Xaa26 Leu Xaa27 Lys
869	Wrong Amino Acid Designator	Xaa28 Pro Asn Met Val Val Xaa29 Ala Cys Gly
869	Wrong Amino Acid Designator	Xaa28 Pro Asn Met Val Val Xaa29 Ala Cys Gly
871	Wrong Amino Acid Designator	Cys His.
873	Wrong Amino Acid Designator	wherein Xaa1 = (Lys or Arg); Xaa2 = (Lys or Ar
873	Wrong Amino Acid Designator	wherein Xaa1 = (Lys or Arg); Xaa2 = (Lys or Ar
873	Wrong Amino Acid Designator	wherein Xaa1 = (Lys or Arg); Xaa2 = (Lys or Ar
873	Wrong Amino Acid Designator	wherein Xaa1 = (Lys or Arg); Xaa2 = (Lys or Ar
873	Wrong Amino Acid Designator	wherein Xaa1 = (Lys or Arg); Xaa2 = (Lys or Ar
873	Wrong Amino Acid Designator	wherein Xaa1 = (Lys or Arg); Xaa2 = (Lys or Ar
873	Wrong Amino Acid Designator	wherein Xaa1 = (Lys or Arg); Xaa2 = (Lys or Ar
873	Wrong Amino Acid Designator	wherein Xaa1 = (Lys or Arg); Xaa2 = (Lys or Ar

The system does not except these notations
 Numbers next to "Xaa". The numbers must be deleted.

[illegible]

Original text

[illegible]

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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Xaa Cys Xaa,

[illegible]

Line	Error	Original text
1126	Wrong Amino Acid Designator	- 18-
1135	Wrong Amino Acid Designator	Xaa Xaa Xaa Xaa Xaa Cys Xaa Cys Xaa,
1138	Wrong Amino Acid Designator	wherein each Xaa independently represents one
1138	Wrong Amino Acid Designator	wherein each Xaa independently represents one
1138	Wrong Amino Acid Designator	wherein each Xaa independently represents one
1138	Wrong Amino Acid Designator	wherein each Xaa independently represents one
1138	Wrong Amino Acid Designator	wherein each Xaa independently represents one
1138	Wrong Amino Acid Designator	wherein each Xaa independently represents one
1139	Wrong Amino Acid Designator	the 20 naturally occurring L-isomer, a-amino a
1139	Wrong Amino Acid Designator	the 20 naturally occurring L-isomer, a-amino a
1139	Wrong Amino Acid Designator	the 20 naturally occurring L-isomer, a-amino a
1139	Wrong Amino Acid Designator	the 20 naturally occurring L-isomer, a-amino a
1139	Wrong Amino Acid Designator	the 20 naturally occurring L-isomer, a-amino a
1192	Wrong Amino Acid Designator	- 19-
1213	Wrong Amino Acid Designator	Cys Gly Cys His.
1148	Entered and Calc. Seq. Length differ	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
1258	Wrong Amino Acid Designator	- 20-
1287	Wrong Amino Acid Designator	Cys Gly Cys His.
1223	Entered and Calc. Seq. Length differ	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
1324	Extra Level-0 Records	- 21-
1390	Wrong Amino Acid Designator	- 22-
1399	Wrong Amino Acid Designator	Cys Gly Cys His.
1329	Entered and Calc. Seq. Length differ	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Page: 5

SEQUENCE MISSING ITEM REPORT

12/10/90

12:32:24

Patent Application US 07/599,543A

Mandatory Identifier that was not found

APPLICATION NUMBER

CLASSIFICATION

OK.